In the Specification:

Please amend the specification as shown:

Please delete the paragraph beginning on page 11, line 30 and replace it with the following paragraph:

Figure 1 Panel A shows an expression cassette in BS14HP-GAP+ vector, which codes for a two species of mRNA synthesized from the constitutive GAP promoters. **See SEQ ID NOS 19, 17, 20, 18, 19 and 20, respectively, in order of appearance, for the disclosed peptides.**

Panel B shows a drawings of the two mature heterologous polypeptides, h679V_H-GGGGS-hMN-14V_K-LEGGGS-hMN-14V_H-6His (Left) **(residues 8-270 of SEQ ID NO: 1)** and hMN-14V_K-GGGQFM-hMN-14V_H-GGGGS-h679V_K-6His (Right) **(residues 7-363 of SEQ ID NO: 2)**, following cleavage of the α factor signal peptides by Kex2 protease.

Panel C shows a drawing of a trivalent protein structure formed by the heterodimerization of polypeptides 1 and 2 possessing two binding sites for CEA and one for HSG.

Panel D shows the amino acid sequence **(SEQ ID NO: 1)** and cDNA sequence **(SEQ ID NO: 9)** of EAEAEFM-h679VH-GGGGS-hMN-14VK-LEGGGS-hMN-14VH-6His **(SEQ ID NO: 1)**.

Panel E shows the amino acid sequence **(SEQ ID NO: 2)** and cDNA sequence **(SEQ ID NO: 10)** of EAEAEF-hMN-14VK-GGGQFM-hMN-14VH-GGGGS-h679VK-6His **(SEQ ID NO: 2)**.

Please delete the paragraph beginning on page 13, line 17 and replace it with the following paragraph:

Figure 10 depicts constructs of SV3 construct and ORF1 and ORF2 polypeptide **(SEQ ID NOS 1 & 2, respectively). The polyhistidine tag in Figure 10A is shown in SEQ ID NO: 20.**

Please delete the paragraph beginning on page 65, line 4 and replace it with the following paragraph:

BS14HP was designed for the constitutive expression of foreign genes in *Pichia pastoris* using the GAP promoter system. Transfection of *P. pastoris* cells with a linearized DNA plasmid (BS14HP-GAP+) results in the stable and site-specific integration of the two DNA segments (Figure 1A) into the GAP locus of the host's chromosome. These two DNA segments contain open reading frames, SEQ ID NO:~~1~~**9** and SEQ ID NO:~~2~~**10**, which codes for polypeptide 1 (SEQ ID NO:~~9~~**1**) and polypeptide 2 (SEQ ID NO:~~10~~**2**) respectively. As each of the two DNA segments also contains nucleotide sequences for the GAP promoter, two mRNA species that encode the amino acid sequences of polypeptide 1 and polypeptide 2 are synthesized in the same host cell.

Please delete the paragraph beginning on page 65, line 21 and replace it with the following paragraph:

The "α-factor," as shown in the schematic of polypeptide 1 and 2 above, represents is a signal peptide that is removed during synthesis and protein transport, which resulting in secretion of the protein (without the signal peptide) into the media. The carboxyl terminal hexa-histadine (6His) sequence **(SEQ ID NO: 20)** allows for rapid and efficient purification of the secreted protein with commercially available immobilized metal affinity chromatography (IMAC) material. hMN-14 V_H represents the amino acid sequence of the variable region of the heavy chain of (V_H region) a humanized monoclonal antibody (Mab) that binds specifically to carcinoembryonic antigen (CEA; Shevitz *et al*, J. Nucl. Med., suppl., 34, 217P, 1993). h679V_K represents the humanized murine monoclonal antibody designated 679 (an antibody of the IgG1, *kappa* class) binds with high affinity to molecules containing the tri-

peptide moiety histamine-succinyl-glycyl (referred to herein as "HSG"; Morel *et al*, Molecular immunology, 27, 995-1000, 1990). The nucleotide sequence pertaining to the variable domains (V_H and V_K) of 679 has been determined (Qu *et al*, unpublished results). Humanized versions of the 679 variable domains (Rossi. *et al*, unpublished results) were used in the design of this construct.

Please delete the paragraph beginning on page 66, line 3 and replace it with the following paragraph:

The short peptide linkers, GGGGS **(SEQ ID NO: 16)**, LEGGGS **(SEQ ID NO: 17)**, GGGQFM **(SEQ ID NO: 18)**, and GGGGS **(SEQ ID NO: 19)**, between the variable domains in the constructs are designed to discourage intra-polypeptide domain pairing. It is anticipated that the two different polypeptides (Figure 1B) would associate with each other noncovalently by pairing the cognate V_H and V_K domains and thereby forming two functional binding sites for CEA and one functional binding site for HSG as shown in Figure 1C.

Please delete the Sequence Listing beginning after page 101 and replace it with the Sequence Listing submitted herewith.